November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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uв-10-736-318-22.rge

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

March 7, 2006, 09:04:19; Search time 14446 Seconds (without alignments) 11509.559 Million cell updates/sec Run on:

Title: Perfect score:

US-10-736-318-22 2925 1 gtttggtatttattggatgc......tcaaatttggactaaatctg 2925 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched:

11766282 5883141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

90 ba: *
90 ln: *
90 loan . *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	ACO21640 Arabidops AF105034 Arabidops AF069468 Arabidops AV088527 Arabidops AK08874 Sequence AK73146 Sequence AK73146 Sequence AK373146 Sequence AK373146 Sequence AK373146 Sequence AR231787 Sinnia el AP081794 Nicotiana AR237881 Sequence AR237881 Sequence AR237881 Sequence AR237881 Sequence AR237881 Sequence BT00553 Triticum AR237878 Sequence BT00553 Zea may8 AK111908 Oryza sat
SUMMARIES	ATACO21640 AF105034 AF065034 AF06846 AF068674 AK573146 AK176721 AK505726 AR176721 AF081794 AF081794 AF081794 AF081794 AF081794 AF081798
08	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
% Query Match Length DB	103904 2294 31063 31063 31075 31175 11175 11176 11186 1187 1187 1187 1181 1181 11
% Query Match	0.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4
Score	13335.21 946.8 956.8 956.8 956.8 956.1 956.1 956.1 956.1 956.1 188.8 188.8 188.8 188.8 188.8 188.8 188.8 188.8 198.8
Result No.	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

clone.

Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov.)

Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene

BAC clone F16B3 is from Arabidopsis chromosome III and is near the molecular marker mi74.

The orientation of the sequence is from SP6 to T7 end of the BAC

AR1237879 Sequence AR137871 Sequence Continuation (19 o AP003214 Oryza sat AR125063 Sequence BT019106 Zea mays BT019106 Zea mays BT019106 Zea mays BT019106 Zea mays BT019105 Sequence G71681 A85715834FM AR249155 Sequence AR249155 Sequence AR245020 Sequence AR245020 Sequence AR24504 Sequence AR25209 Sequence I66494 Sequence I66494 Sequence I66494 Sequence AR25209 Sequence	AC087566 Mus muscu AX346599 Sequence AC104922 Mus muscu
AK137879 AK112014 AR237871 AR237871 AP003201 AP003214 AX155063 BD273096 BD273096 G71612 AX149155 G71681 BV007175 AR2455209 AR252099	AC087566 AX346599 AC104922
0 1 1 1 1 1 2 2 2 2 2 3 2 3 3 3 3 3 3 3 3	14 9 1
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179.6 176.4 163.8 163.8 163.8 163.8 120.8 138.8 138.8 118.4 118.4 118.4 108.6 90.8 77.8 77.8 77.8 77.8 77.8 77.6 77.8	70.4
119 22222222222222222222222222222222222	444
0 00 0	υ

ALIGNMENTS

RESULT 1 ATAC021640	
LOCUS	ATAC021640 103904 bp DNA linear PLN 30-OCT-2002
DEFINITION	Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence,
	complete sequence.
ACCESSION	AC021640
VERSION	AC021640.7 GI:12408747
KEYWORDS	HTG.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
	<pre>Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;</pre>
	Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons;
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 103904)
AUTHORS	Lin, X., Kaul, S., Town, C.D., Benito, MI., Creasy, T.H., Haas, B.,
	<pre>Wu,D., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,</pre>
	Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.
TITLE	Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 103904)
AUTHORS	Lin, X. and Kaul, S.
TITLE	Direct Submission
JOURNAL	Submitted (18-JAN-2000) The Institute for Genomic Research, 9712
	Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
REFERENCE	3 (bases 1 to 103904)
AUTHORS	Lin, X.
TITLE	Direct Submission
JOURNAL	Submitted (24-JAN-2001) The Institute for Genomic Research, 9712
	Medical Center Dr., Rockville, MD 20850, USA
COMMENT	On Jan 24, 2001 this sequence version replaced gi:12280770. Address all correspondence to:at@tigr.org

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(http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TiGR (http://www.tigr.org/tdb/at/at.html).
Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy.). Simple repeats are identified by repeatmasker (Arian Smit, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html).
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REFERENCE 2 (bases I to 1163) AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, YP., Flavell, R. and Feldmann, K. TITLE Unpublished JOURNAL Grow Arabidopsis thaliana JOURNAL Grower, V., Troukhan, M., Alexandrov, N., Lu, YP., Flavell, R. and REFERENCE Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Mallbu, CA 90265, USA COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TigR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent are 3'-truncated; approximately two percent represent alternative spilce variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequences are derived from the Ws or LAGI cotypes and therefore may contain and of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAGI ecotypes and therefore may contain polymorphisms when compared to sequence in contain of the should contain of the contain premature of sequences are derived from the Ws or LAGI ecotypes and therefore	full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly. PEATURES Location/Qualifiers Location/Qualifiers Location-Corporation of clones, and sequence assembly.	/ AD XXEE= TATA AND SOLUTION TO THE STANDARY OF THE STANDARY O	Db 671 Tricccedectriccarrachedecedriccarrachedecreracecerrachedrata 730 Qy 521 GCGCTG-TTATAGTGCCAATTCATTCACAACTCATATAGGCTTTTGTTCATGGAAGCG 579 Db 731 GCGCTGTTTATAGTGCCAATTCATTCACAACTCATATAGGTCTTTTGTTCATGGAAGCG 790 Qy 580 ATATGGACGGCGAACATCATTCACACTCATATAGGTCTTTTGTTCATGGAAGCG 790 Qy 640 GGATACCATACACTCATGACTGCATCCATGGCACATCTGGCAGTAATGGGTGCA 639 Qy 640 GGATACCATACGATACACCACACACACACACACACATATGGTCATTATACCATATGG 699 Db 851 GGATACCATACGATACACACACACACACACACACACACAC
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                Karunanandaa, B., Post-Beittenmiller, M., Venkatramesh, M., Kishore, G.M., Thorne, G.M. and Ledeaux, J. Transgenic plants containing altered levels of steroid compounds Patent: WO 02061072-33 08-AUG-2002; Monsanto Technology LLC (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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Pred. No. 3.3e-76;
0; Mismatches 10
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 940 TAAATGTTTGATGATCTTTGC
                     1123 TAAATGTTTGATGATCTTTCC
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Best Local Similarity 97.6%;
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                                                                                                                                                                                                                                                                                                                                                                                Unknown.
Unclassified.
Unclassified.
I (Dases 1 to 1175)

Karumanadas, B., Post-Beittenmiller, M., Venkatramesh, M.,
Kishore, G.M., Thorne, G.M. and LeDeaux, J.R.
Transgenic plants containing altered levels of steroid compounds
Patent: US 6822142-A 3 23 -WOV-2004;
Monsanto Company; St. Louis, MO
Location/Qualifiers
                               521 GCGCTG-TTATAGTGCCAATTCATTTCACAACTCATATAGGTCTTTTGTTCATGGAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     703 GCGCTGTTTATAGTGCCAATTCATTTCACAACTCATATAGGTCTTTTGTTCATGGAAGCG
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Submitted (16-5EP-2004) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:mseki@gsc.riken.jp, 100045, Japan (B-mail:mseki@gsc.riken.jp, 100045, Japan (B-mail:mseki@gsc.riken.jp, 100045-503-9625, Pax:81-45-503-9586)

An Arabidopsis full-langth cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15.707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This clone is in a modified pluescript vector.

Pleage visit our web site (http://rarge.gsc.riken.jp/) for further
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TVSBSMIERGWTKCFASIGEFGWILYFVYIAIYLVFVEFGIYWMRRELHDIKPLXYL
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1063 GTCTCTCTCAACCTTTCCAATTATATATTGTTACAAACATTTGCTGTCTAGTTTAAAACATG 1122
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Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales; Brassicaceae, Arabidopsis.
                                                                          GTCTCTCTCAACCTTTCCAATTATATTGTTACAAACATTTGCTGTCTAGTTTAAAACATG

    1113

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db xref="taxon:3702"

/chromosome="3"

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/gene="At3g02580"
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NYLAGTLIYISGPLWCFUDFTSFYNRIVLSHLLPANLWEPLPHFLQTWLR
NYLAGTLLYIISGPLWCFYIYYRKINVYLPKDAIPTIKAMRLQMFVAMKAMPWYTLLP
TVSESMIERGWTKCFASIGFFCWILYFVYIAIYUFVEFGIYWMHRELHDIKFLYKYL
HATHIYNKQNTLSPFAGLAFHPVDGILQAVPHVIALPIVPIHFTTHIGLLFMBAIWA
ANIHOCIHGNIWPVMGAGYHTIHHTTYKHNYGHYTINMDWMFGSLRDPLLEEDDNKDS
FKKAE"
                                                                                                                                                                                                                                                                         Gachotte, D., Husselstein, T., Bard, M., Lacroute, F. and Benveniste, P. Isolation and characterization of an Arabidopsis thaliana cDNA encoding a delta 7-sterol-C-5-desaturase by functional complementation of a defective yeast mutant plant J. 9 (3), 391-398 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-JUL-1995) D. Gachotte, Institut de Biologie
Moleculaire Plantes, Enzymologie Moleculaire et Cellulaire,
Institut de botanique 28, rue Goethe, F- 67083 Strasbourg, FRANCE
Location/Qualifiers
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larity 97.6%; Pred. No. 3.3e-76;
Conservative 0; Mismatches 10; Indels 2
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/product="sterol_C5-desaturase"
/protein_id="CAA62079.1"
/db_xref="G1:1061038"
/db_xref="G0A:Q39208"
/db_xref="UniProt/TrEMBL:Q39208"
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/mol_type="mRNA"
/db_xref="taxon:3702"
       ATRNASCSD 1175 bp mRNA A.thaliana mRNA for sterol-CS-desaturase.
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                              A.thaliana mRNA for sterol-C5-desat
X90454
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sterol-C5-desaturase gene.
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NITHOCIHGNIWPVMGAGYHTIHHTTYKHNYGHYTIWMDWMFGSLRDPLLBEDDNKDS
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Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 421 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations A (CH)
                                                                                                                                                                                              GGATACCATACGATACACCACACACATACAAGCATAACTATGGTCATTATACCATATGG
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Pred. No. 4.7e-70;
0; Mismatches 3;
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/organism="Arabidopsis thaliana"
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Best Local Similarity 98.9
Matches 452; Conservative
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                                                                                                                                                       GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA
                                                                                                                                                                                                                   GCCATGGTACACTCTTCTTCCAACTGTCTCCGAGAGTATGATGATGAACGTGGTTGGACCAA
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AUTHORS
TITLE
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1155 bp mRNA linear PLN 19-MAY-1999 tabacum sterol-C5(6)-desaturase mRNA, complete cds.
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GGVLLYFISGFLWCFYIYHLKRNVYIPKDALPSNKAMLLQISVAMKAMPWYCALPSLS
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HHIYNKQNTLSFPGALFHPLDGILQAVPHVVALLLIVPWHSCTHIALIFLEALWTANI
HDCIHGKVPFVWGAGYHTIHHRIYRHNYGHYTIWMDWMFGTLRDPVEEDAKKM"
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739 GGGCATTATACAGTTTGGATGGACTGGATGTTCGGTACCCTTCGTGATCCTTTGGAAGAG 798
                                                                                                                                                                                                                                                                                                                       Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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Submitted (30-JUL-1998) Plant Molecular Biology Institute, Centre
National de la Recherche Scientifique, 28 rue Goethe, Strasbourg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2153 CACTIGACCAITICAACIGGIICCICIGIIIICCICIACAIAGCICICIAITIAG
                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1155)
Husselstein, T., Schaller, H., Gachotte, D., and Benveniste, P.
Deltar sterol-C5-desaturase; molecular characterization and
functional expression of wild-type and mutant alleles
Plant Mol. Biol. 39 (5), 891-906 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tisue type="calli derived from leaf protoplasts"
103. .918
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/db_xref="G1:4140398"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 195;
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61.1%; Pred. No. 1.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1155
/organism="Nicotiana tabacum"
                                                                                                                                                                                                                                                                                   tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db xref="taxon:4097
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Matches 441; Conservative
                                       2691 AAAGACA 2697
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                                                                                 799 GAGGCCA
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                                                                                                                                                                                                                                                              /product="delta7 sterol C-5 desaturase"
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HHINKQNTLSFPGALAFHALDGILQA1PHYVALFLVPTHRWTHILLLEMBAIWTANI
HDCIHGKFWPVMGAGYHTIHHTTYRHNYGHYTVWMDWMFGTLRDPLEEEBAKOM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2271 GCATCTCCATGCTACCCATCATATGTACAAGCAAAAACACACTCTCTCCATTTGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.8%; Score 228.2; DB 15; Length 1104; 60.9%; Pred. No. 1.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
    (E-mail:brassin@affrc.go.jp, Tel:81-29-838-8392)
Fax:81-29-838-8392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.5e-32;
0; Mismatches 198;

    1104
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/mol_type="mRNA"
/db_xref="taxon:34245"

                                     Location/Qualifiers
                                                                                                                                                                                       1. .816
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/note="STB1"
/codon_start=1
                                                                                                                                                  l. .1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                               .816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Matches 443;
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xref="GI:4426627"

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/translation="MDDYLNLFIEETSFYNRVVLGTFLPESWWGPLPHWFQGWLRNYI
GGVLLYFISGFLWCFYIYRLKRNVYIPKDAIPSNRAWLQCYGWMKAMPFYCALDSLS
EWHIVNGWTKCFSRISDVGWLSYLIYMAVYLVIVEFGIYWMHRELHDIKLLYKYLHAT
HHIYNKQNTLSFFGLAFHPLDGILQAVPHVVALFLLFEHFTTHIALLFIEAIWTANI
HDCKHAKVWPVMGAGYHTIHHTTYRHNYGHYTIWMDWMFGTLRDPVEDEVKKM"
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Pred. No. 8.4e-31;
0; Mismatches 172; Indels
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1 (bases 1 to 1447)
Famodu,0.0. and Rafalski,J.A.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons, asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1148)
Husselstein,T., Schaller,H., Gachotte,D. and Benveniste,P.
Dellar-sterol-C5-desaturase: molecular characterization and functional expression of wild-type and mutant alleles
Plant Mol. Biol. 39 (5), 891-906 (1999)
                                                                   TGTCAAAGCTATATGTTCTCAATTCTAAATTCAAGAGCTTGTATCAATGGTGACTTCTTTA
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                       663 AGTGCCACACGTTGTAGCTCTATTATTGGTGCCAATGCATTTCAGTACACACATAGCACT
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/mol_type="mRNA"
/culTivar="xanthi SH6"
/db xref="taxon:4097"
/cell_type="protoplast (calli)"
/tisue_type="leaf"
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                                                                                                                                                                                                                                                                         86;
                                                                                                                                                                                                                                 Length 1447;
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Sterol metabolism enzymes
Patent: US 6465717-A 27 15-OCT-2002;
B. I. du Pont de Nemours and Company; Wilmington,
EPX;
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ilarity 61.3%; Pred. No. 6.1e-28;
Conservative 0; Mismatches 166;
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Unclassified.
1 (bases 1 to 1210)
Famodu,O.O. and Rafalski,J.A.
Sterol metabolism enzymes
Patent: US 6465717-A 29 15-OCT-2002;
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US 6465717.
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/organism="unknown"
/mol_type="genomic DNA"
                                                                                                    Location/Qualifiers
1. .1447
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Sequence 29 from patent
AR237881
AR237881.1 GI:27282714
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Trificum aestivum (bread wheat)

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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Poaceae;

Socialeae; Trificaea; Trificum.

Toaceae 1 to 1210)

Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,

Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
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59.8%; Pred. No. 4.9e-25;
*ive 0; Mismatches 175; Indels

    1210
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    /mol_type="genomic DNA"

Location/Qualifiers
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BT009523.1 GI:32129074
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Matches 389; Conservative
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Direct Submission
Submitted (20-UUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
                                                                                                                                                                                                                                                                                                              188 AGATGCTCTCCTACAGTAGAAGCTATGAAGAAGCAAATAATTGTTGCATCAAAAGGCTAT 247
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Best Local Similarity 59.8%; Pred. No. 4.9e-25;
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps
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702 CACAACTATGGCCACTACACGTGTGGATGGACTGGCTGTTTGGCACCT 751
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                                                                 Location/Qualifiers
1. .1210
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/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wx1.pk0107.a5:fis"
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AAA66689
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                            and encoding polymuclectides that impart at least one dwf7 mutant phenotype when expressed in a plant. The polymucleotide sequences encoding the mutant dwf7 proteins are useful for producing transgenic plants from transformed plant calls. The polymucleotide sequences are useful for altering the sterol composition of a plant relative to the wild-type plant. The transgenic plant has less cholesterol or increased atealor production relative to the wild-type plant. The mutant sequences are also useful for isolating or creating other mutant cell gene alleles and for detecting plant regulatory defects which can affect plant growth. The present sequence encodes Arabidopsis thaliana dwf7 homologue protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                     present invention relates to the isolation of dwarf7 (dwf7) mutants
                                                                                                   Novel isolated dwf7 polynucleotide for altering sterol composition of a plant, by introducing polynucleotide into plant cell to produce transformed plant cell and producing transgenic plant from transformed
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The invention relates to an isolated dwarf? (dwf?) polynucleotide that imparts at least one dwf? mutant phenotype when expressed in a plant. The imparts at least one dwf? mutant phenotype when expressed in a plant. The convention also relates to a recombinant vector comprising the dwf? polynucleotide and control elements that are operably linked to the colynucleotide where a coding sequence within the polynucleotide can be cranscribed and translated in a host cell, and at least one of the control elements is heterologus to the coding sequence, a host cell control elements is heterologus to the coding sequence, a host cell control elements is heterologus to the coding sequence, a host cell control elements is heterologus to the coding sequence, a control element of the transgenic plant and a method of producing a transgenic plant and a method of altering the compression of a plant relative to the wild-type plant. The dwf? control composition of a plant relative to the wild-type plant. The dwf? C plants which display at least one dwf? phenotype, so that the resulting conserving other mutant alleles and for enableding or in industrial applications. The dwf? polynucleotides are useful for isolating or creating other mutant alleles and for enhancing certain features such as increased seed production. They are also useful for conferring desired tratts on any plant, for altering secon content and for providing a tool for increasing or reducing cholesterol content and for providing a tool for increasing or reducing cholesterol content and for providing a tool for
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TCTCGTGACTCTTATTAAAACCTTTCTAATCACTTTGGTGGAATTAAAAACATGACTGCA
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cholesterol; ds.

(first entry)

Location/Qualifiers
143. .1709
/*tag= a
/product= "dwf7"

/number= 1 369. .735

*tag= b

143. .368

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Gene encoding Arabidopsis thaliana dwf7 protein.
                                                Dwarf7; dwf7; plant cell; sterol composition;
plant regulatory defect; plant growth; plant;
                                                                                    Arabidopsis thallana
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                                     TTAGTTCTATTTCTTGCTTGGTTTCTTCTATTTTTGTGGTTAGAATCCATTCCTACGAGA
                                                                                     AAGGCAATGCTTTTGCAAATATACGTGATGAAGGCTATGGCTTGGTACACTCTTCTT
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                                                                        AAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTATGCCTTTGGTACACTCTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated dwf7 polynucleotide for altering sterol composition of a plant, by introducing polynucleotide into plant cell to produce transformed plant cell and producing transgenic plant from transformed
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Pred. No. 5.8e-206;
0; Mismatches 1; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1889 BP; 466 A; 385 C; 352 G; 686 T; 0 U; 0 Other;
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Best Local Similarity 99.6%;
Matches 958; Conservative
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(FELD/) FELDMANN K A.
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P-PSDB; AAU99577.
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ABK89915 standard; DNA; 1889

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The invention relates to an isolated dwarf7 (dwf7) polynucleotide that imparts at least one dwf7 mutant phenotype when expressed in a plant. The invention also relates to a recombinant vector comprising the dwf7 polynucleotide and control elements that are operably linked to the polynucleotide and control elements that are operably linked to the polynucleotide and control elements is netrologous to the coding sequence, a nost call transformed with the recombinant vector above, a method of producing a control elements is heterologus to the coding sequence, a host call transformed with the recombinant vector above, a method of producing a control elements is heterologus to the wild-type plant. The dwf7 polynucleotides and polypeptides are useful for producing transgenic plants which display at least one dwf7 phenotype, so that the resulting plants have altered structure or morphology. The transgenic plants are useful in plant breeding, in agricultural production or in industrial applications. The dwf7 polynucleotides are useful for resoluting or solution are mutant alleles and for enhancing certain features such applications. The dwf7 polynucleotides are useful for conferring and increased seed production. They are also useful for conferring desired increased seed production. They are also useful for conferring or reducing cholesterol content and for providing a tool for studying the biosynthesis of brassinosteroids. The dwf7 control element is useful as a plant promoter to express any protein of interest in a transgenic plant, particularly to express a protein involved in the brochmical applications, e.g., regulation of setrol superimental or industrial biochemical applications. This sequence represents thale cress dwarf7 (dwf7) DNA, used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated dwarf 7 (dwf?) polynucleotide, useful for conferring desired traits on essentially any plant and for altering sterol composition of a plant thus increasing or reducing cholesterol content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCATGCCACCCATCATATCTACAAGCAGAATACACTCTCTCCATTTGCCGGTAAGTG 120
                                            Thale cress, dwarf7; dwf7; sterol; plant breeding; agricultural production; flowering; leaf production; fruit production; branching; seed production; cholesterol; brassinosteroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GITIGGIAITIAITIGGATGCACAGAGAGCTTCATGACATTAAGCCTCTCTATAAGTATCT
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              cress dwarf7 (dwf7) DNA
                                                                                                                                                                                                                                                                     02-FEB-2000; 2000US-0179901P. 02-FEB-2001; 2001US-00775879.
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P-PSDB; ADQ28842.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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The invention describes a plant (I) comprising DNA encoding a polypeptide (P1) with 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity and a polypeptide (P2) with steroid pathway enzyme activity such as squalene epoxidase, sterol methyl transferase I, sterol C4-demethylase, obtusifoliol C14alpha-demethylase, sterol C5-desaturase or sterol methyl transferase I is terol C4-demethylase, cransferase I is not recombinant vector expressing P1 is useful for increasing the formation of steroid pathway products in a transformed host cell as compared to an otherwise identical nortransformed host cell. (I), a plant containing a cell transformed using a recombinant vector (II) is useful for producing a plant by sexually crossing (I), (II) or (III) with a non-transformed plant. A cholesterol lowering composition (IV) containing at least one sterol pathway product (V), a food product containing (V), and a pharmaceutical composition containing (V) is useful for lowering the plasma
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                                                                                                                          GTCTCTCTCAACCTTTCCAATTATATTGTTACAAACATTTGCTGTTTAAAACATG
                                                                       GTIGTIGTICATAGTTCAGCCTTTCTTGTTCTTTTTCTTCTTCTTCTTATTCATGT
                                                    GITGITGITGITCAAAGITTCAGCCITTCITGITCITTTTTCTTCTTCTTATTCATGI
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concentration of low density lipoprotein cholesterol or for treating or preventing an elevated plasma concentration of low density lipoprotein cholesterol. (1), or a transgenic plant is useful for making a food additive composition by obtaining oil containing a steroid pathway product from seed of (1), or a transgenic plant and mixing the oil with an edible solublising agent, a dispersant, and optionally an antioxidant. (V) is useful for reducing the concentration of low density lipoprotein cholesterol in plasma. (I) has improved nutritional characteristics. This sequence represents an Arabidopsis thaliana sterol C5-desaturase
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                                                                                                                                                                                                           Length 1175;
                                                                                                                                                                           Sequence 1175 BP; 300 A; 265 C; 227 G; 383 T; 0 U; 0 Other;
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                                                                                                                                                                                                           ; DB 6;
1.5e-97;
                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                         Score 461;
Pred. No. 1
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Best Local Similarity 97.6%;
Matches 489; Conservative
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2082 GCCTTGGTACACTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141
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739 CATAACTATGGTCATTATACCATATGGATGGATGTTTGGCTCTCTTAGGGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 AGATGCTATTCCCTCTCAAAGAGCCATGCTCTTGCAATATCTGTTGCTATGAAAGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corn; wheat; rice; soybean; plant; gene; ss; sterol metabolism;
sterol delta 7; reductase; sterol C5 desaturase.
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                                                                                                                                                                                                                          2682 TTAGCAGAAAAGACAGTTTCAAGGAGAAAGAAAGTGAGAA 2723
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                                                                                                                                                                                                                                                                                         799 CICTTAGAAGAIGACGACAAGAGACAGCTTCAAGAAAGCA
                                                                                                        2622 CATAACTATGGTCATTATACCATATGGATGGACTGGATGTT
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Best Local Similarity 61.3%;
Matches 399; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes repressed polynucleotides in the plant cell with an detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to ablotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGG 2381
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                                                                                                                                                                                                                                                                                                                                                                                       Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.9%; Score 347.2; DB 6; Length 846; 72.4%; Pred. No. 6e-71; Live 0; Mismatches 108; Indels 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 144; SEQ ID NO 421; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 846 BP; 222 A; 198 C; 170 G; 256 T; 0 U; 0 Other;
                                                                                                                                                                         ) SCRIPPS RES INST.
) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                  Wang X,
                                          24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                  Harper JF, Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 508; Conserva
                                                                                                                                                                                                                                                                                                                                WPI; 2002-304127/34.
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2202 TCTIGITTTAGTIGAGTITATGATTTATIGGGTICACAAAGAGCTICATGACATTAAATT 2261
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                                                                                                           New polynucleotide encoding a transcription factor polypeptide, useful in genetic mapping for plant breeding.
                                                                                                                                                                                          The invention relates to a polynucleotide which encodes a transcription factor. The nucleic acid fragment is useful in genetic mapping for plant breeding. The present sequence is sterol-C5-desaturase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 AGATGCTATTCCCTCTCAAAGAGCCATGCTCTTGCAAATATCTGTTGCTATGAAAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                       2082 GCCTTGGTACACTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTCGACCAA
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                                                                                                                                                                                                                                                                                        Query Match 7.0%; Score 203.4; DB 12; Length 1447; Best Local Similarity 61.3%; Pred. No. 3.4e-37; Matches 399; Conservative 0; Mismatches 166; Indels 86;
                                                                                                                                                                                                                                                           Sequence 1447 BP; 444 A; 283 C; 294 G; 426 T; 0 U; 0 Other;
                                 Shen JB;
                                 Rafalski JA,
                                                                                                                                                             Claim 2; SEQ ID NO 27; 43pp; English.
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                                                               WPI; 2004-052051/05.
P-PSDB; ADI19007.
                                 Orozco
   (SHEN/) SHEN J B.
                               Pamodu 00,
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AC ADI4
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                                                                                                              615
                                                                                                                                                                                                                                                                                                                         649
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436 GTGCTATCCTAGATTATATGTTGGTTGGCTTGCATACCTTGTGTATTTAGCAATTTA
                                                                                             TCTTGTTTTAGTTGAGTTTTATGATTTGGGTTCACAAAGAGCTTCATGACATTAAATT
                                                                                                                                                                                556 GCTTTACAAATATCTTCATGCTACCATCACATCTACAATAAACAGAACACTCTCTCCCC
                                                                                                                                                                                                                                                                                        2382 TGACTICTITACTIGATGITITICGGGITITICAGGCTCGCATICCATCCGCTGGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                         2142 AIGTIACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTTA
                                                                                                                                                             2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAAGCAAAACACACTCTCTCC
                                                                                                                                                                                                                                                                                                                      616 TTTTGCTGGTTTG--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor; genetic mapping; plant breeding; sterol-C5-desaturase; soybean; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107. .916
/*tag= a
/product= "Sterol-C5-desaturase"
/partial
/note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean sterol-C5-desaturase cDNA #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                         629 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI19006 standard; cDNA; 1447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FAMO/) PAMODU O O.
(OROZ/) OROZCO E M.
(RAFA/) RAFALSKI J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003229914-A1
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19-NOV-1999;
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2081

Gaps

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435

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ADI19006

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Gaps

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409

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WPI; 2004-090562/09
                                                                                                  P-PSDB; ADI45357
                              US2004010815-A1.
                                                       LANGE
                     haeme; yield
                          Oryza sativa
                                             26-SEP-2001;
04-APR-2002;
22-APR-2004
                                   15-JAN-2004
                                                                                      Lange BM,
Goff SA,
                                                                          (MOUG/)
(PROV/)
(RICK/)
                                                       LANG/)
                                                                (GLAZ/)
                                                                     (KATA/)
                                                           (BRIG/)
(COOP/)
                                                                                 ZHUT/)
                                                         GHAS/)
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2623 ATAACTATGGTCATTATACCATATGGATGGACTGGATGTTTGGCTCTTATGGTTCCTT 2682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wheat; isoprenoid biosynthesis; ss; plant; isopentenyl diphosphate; IPP;
                                                                                                 segdata uspto.gov/seguence.html?DocID=20040010815. The present seguence is a Rice isoprenoid biosynthesis- associated cDNA of the invention.
             as markers and probes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGTTTTAGTTTTATGATTTTATTGGGTTCACAAAGAGCTTCATGACATTAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 ACATTGCTCTCTTGTTCATAGAGGCCGTGTGGACAACTAACATCCATGACTGCATTCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTTGGTACACTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTATA
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acid molecules are useful for targeted gene disruption, as its and probes. Note: The sequence data for this patent did
                                                                                                                                                                                                                                                                                   79;
                                                                                                                                                                                                                                DB 12; Length 833;
                                                                                                                                                                            Sequence 833 BP; 199 A; 226 C; 193 G; 215 T; 0 U; 0 Other.
                                                                                                                                                                                                                                                           Pred. No. 5.3e-34;
0; Mismatches 191; Indels
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                                                                                                                                                                                                                                Score 189.4; DB 12
Pred. No. 5.3e-34;
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                                                                                                                                                                                                                                                                                        393; Conservative
                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                     Query Match
     nucleic
                                                                                                                                                                                                                                                                                        Matches
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     8866666888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a polymucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide encoding a polypeptide comprising an amino acid sequence convoluted in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polypeptide involved in or associated with the biosynthesis of isoprenoids in a plant, an expression cassette comprising the polymucleotide, a host cell comprising the expression cassette. The polypeptides and polymucleotides include those associated with the biosynthesis of short-chain plastid cassette. The polypeptides and polymucleotides include those associated with the biosynthesis of short-chain plastid alondoil (DMAPP), the biosynthesis of short-chain plastid alondoil (DMAPP), the biosynthesis of short-chain plastid cancercl and polymucleotides include those associated caretorlandor and/or abscisic acids, the biosynthesis of ubiquinone with the biosynthesis of short-chain plastid pathway, placecrol and brassinosteroid metabolism, biosynthesis of ubiquinone, biosynthesis of ubiquinone, biosynthesis of ubiquinone, biosynthesis of conception and sesquiterpenes, protein prenylation, and biosynthesis of chorophyll or haseme. Also disclosed are banana, wheat and corn homologues of some of the rice polymucleotides are useful for producing transgenic plants, where the gene can an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce a better quality product than the corresponding wild-type plant. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.
                                                                                                      Rice; isoprenoid biosynthesis; 88; gene; plant; isopentenyl diphosphate; IPP; dimethylallyl alcohol; DWAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone; phylloquinone; mevalonate pathway; phytosterol; brassinosteroid; ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll;
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Moughamer T, Provart N, Ricke
                                                        Rice isoprenoid biosynthesis-associated cDNA #144
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Katagiri F, Kreps J,
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        (first entry)
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KREPS J.
MOUGHAMER T.
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COOPER B.
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RICKE D.
ZHU T.
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The invention relates to a polymucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide encoding a polymeptide comprising a nucleotide encoding a polymeptide comprising an anino acid sequence involved in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polymeptide involved in or expression cassette comprising the polymeptides and isoparthesis of isoprenoids in a plant, an expression cassette comprising the polymucleotide, a host cell comprising the polymptides and blosynthesis of isoparthesis of expression cassette. The polymptides and polymucleotides include those associated with the biosynthesis of isopartenyl diphosphate (IPP) and dimethylallyl alcohol (DMAPP), the biosynthesis of short-chain plastid alcohol (DMAPP), the biosynthesis of short-chain plastid corrected and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or absciste acids, the biosynthesis of tocopherols, phytosterol and brassinosteroid metabolism, biosynthesis of ubiquinone, corrected and brassinosteroid metabolism, biosynthesis of ubiquinone, biosynthesis of chlorophyll or harmen. Also disclosed are banana, wheat and corn homologues of some of the rice polymucleotides. The plants are useful for producing transgenic plants, where the corresponding gene has been disrupted, e.g. to result in a loss, a decrease or an alteration in the function of the product and better quality product than the corresponding wild-type plant. The corresponding are useful for targeted gene disruption, as well as markers and probes. Note: The sequence dence disruption, as well as markers and probes. Note: The sequence date for this patent did not correct or directly from USPTO at a general correction, the product han the corresponding wild-type plant, and a corresponding are useful for targeted gene disruption, as well as markers and probes. Note: The sequence date for this patent did not correct benefit and decreased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.
                                                                  ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll;
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dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone; phylloquinone; mevalonate pathway; phytosterol; brassinosteroid;
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rovart N, Ricke D;
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eps J, Moughamer T, Provart N,
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Katagiri F, Kreps J,
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04-APR-2002; 2002US-0370620P.
04-APR-2002; 2002US-0370743P.
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KREPS J.
MOUGHAMER T.
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Goff SA,
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                                                                                         2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTAT 2081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corn; wheat, rice; soybean; plant, gene; ss; sterol metabolism; sterol delta 7; reductase; sterol C5 desaturase.
                                                            86;
                             Length 1135;
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Sequence 1135 BP; 243 A; 292 C; 296 G; 304 T; 0 U; 0 Other;
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                                                            Indels
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                                               Pred. No. 1.2e-33;
0; Mismatches 175;
                             DB 12;
                                             1.2e-33;
                             Score 188;
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                                           59.88;
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                                           Best Local Similarity 59.8
Matches 389; Conservative
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                             Query Match
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2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTTA 2201
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                        CATAACTATGGTCATTATACCATATGGATGGACTGGATGTTTGGCTCTCT
                                                      702 CACAACTATGGCCACTACACCGTGTGGATGGACTGGCTGTTTGGCACCCT
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1 Similarity 59.8%; Pred. No. 1.3e-33;
389; Conservative 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription factor; genetic mapping; plant breeding; sterol-C5-desaturase; wheat; gene; ss.
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/product= "Sterol-C5-desaturase"
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(OROZ/) OROZCO E M.
(RAFA/) RAFALSKI J A.
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0; Mismatches 175;
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98US-0109283P
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Matches 389; Conservative
                                                                                                               Rafalski JA;
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Best Local Similarity 59.8°
Matches 388; Conservative
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          TCTTGTTTTAGTTGAGTTTATGATTTATTGGGTTCACAAAGAGCTTCATGACATTAAATT
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P-PSDB; ABG73988
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sequences may also be useful for producing a transgenic plant, by transforming a plant cell with the cDNA sequence and regenerating a transgenic plant from the transformed plant cell. The nucleotide sequence is useful for obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding a sterol delta-7 reductase or a sterol-c5 desaturase polypeptide. Probes derived from the nucleotide sequence of the invention may be useful for physical mapping. The present sequence represents a cDNA sequence encoding a sterol metabolism enzyme of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 ACATCGCTCTCGTGTTCTTGGAGGGCGTGTGGACGACGACAAACATCCACGACTGCATTCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 GCAAGGTATGGCCAGTCATGGGCGCTGGGTATCACACCATCCACCATCCACCATACCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2023 GAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GATGCCATCCCCACAAATGAAGCTATGAAGAAGCAAATAGCTGTAGCATCCAAGGCTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 TGTTACTTTAATATCAGCGAAATGGGTTTTTTCTGCATACCTTTGTTATATGGCTATGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAAGCAAAACACACTCTCTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTATACAAACATCTGCATGCGACCCACCATATTTACAACAAGGAGAACACCCTTGTTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2383 GACTICTITACTIGAIGITITITCGGGTTTTTCAGGGCTCGCAITCCAICCGCTGGACGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 TTCTGCAAGCGATACCGCATGTGCTTGCGCTCTTCCTCCTCCCAACGCACTTCAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 187; DB 8; Length 911;
Pred. No. 2e-33;
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                                                                                                                                                                                                                                                                                                                                 Sequence 911 BP; 222 A; 214 C; 217 G; 258 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 175; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAAGCAAAACACACTCTCTCCA 2322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2443 TACTICAGGCIAIACCGCACGIGAIAGCGCIGITIAIAGIGCCGAIICAICICICAIAACAC 2502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide encoding a transcription factor polypeptide, useful in genetic mapping for plant breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATACAAACATCTGCATGCGACCCACCATATTTACAACAAGGAGAACACCTTGTCTCCG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a polynucleotide which encodes a transcription factor. The nucleic acid fragment is useful in genetic mapping for plant breeding. The present sequence is sterol-C5-desaturase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGCCATCCCCACAAATGAAGCTATGAAGAAGCAAATAGCTGTAGCATCCAAGGCTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.4%; Score 187; DB 12; Length 911;
Best Local Similarity 59.8%; Pred. No. 2e-33;
Matches 388; Conservative 0; Mismatches 175; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 911 BP; 222 A; 214 C; 217 G; 258 T; 0 U; 0 Other;
                                                            /*tag= a
/product= "Sterol-C5-desaturase"
/partial
/note= "No start and stop codon"
                                                                                                                                                                                                                                                                                                            Shen JB;
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 23; 43pp; English.
                                                                                                                                                                                                                                                                                                            Rafalski JA,
                                   Location/Qualifiers 74. .646
                                                                                                                                                                              21-AUG-2002; 2002US-00224880
                                                                                                                                                                                                       98US-0109283P.
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OROZCO E M.
RAFALSKI J A.
SHEN J B.
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P-PSDB; ADI19003.
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19-NOV-1999;
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DRS64230 WS0335.C2
DR069207 RTAL1, 7 E
CR340394 RTAL1, 7 E
CR30136 RHOHL 43
CR3136598 BLO1N0360
CD434877 EL01N0329
CA252633 SCVPFH114
DR69736 WS00948.B
CP272845 EST3051 E
DR394443 EST3051 E
DR394443 EST3051 E
DR6955 RS00947.B
CL95724 OBIFCC000
CX09951 RECM0308
DR10956 RTS1 4 A0
CF227924 PtaXM0006
CX051357 RS1744994
CM84525 010811AAS
CD918892 OV.111G01
BW665027 PW685027
CX659607 PO01032G0
CX659607 PO01032G0
CX659607 PO01032G0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Special yarrange streptophyta; Embryophyta; Tracheophyta; Special Spec
WS00753.C
WS0335.C2
RTAL1 7 E
POPSC0037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sessions A Applied Trait Genetics Syngeria Biotechnology Inc. Syngeria Biotechnology Inc. Syngeria Biotechnology Inc. Syngeria allen. sessions@syngenta.com Email: allen. sessions@syngenta.com Email: allen. sessions@syngenta.com Syngeria allen. sessions@syngenta.com as Email: allen. sessions@syngenta.com et border flanking sequences Syngeria Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xrefe"taxon:3702"
/clone="SAIL 1124 H08.v1"
/clone="SAIL Collection"
/note="T--DNA left border sequences were isolated using a
modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 355.4; DB 10; Length 940;
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/mol_type="genomic DNA"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                         DR584230
DR584230
CBA40394
CN130796
DR361343
CD436598
CD434877
CD434877
DR46526
CC7272845
DR46526
CL957247
CC099651
DR1096651
CR277924
CC098652
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Class: TDNA tagged.
Location/Qualifiers
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SOURCE
ORGANISM
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JOURNAL
PUBMED
COMMENT
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VERSION
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AUTHORS
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CL460967
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CD823918 BN25.047B
BX384971 SALK 1348
CD823327 BN25.048G
CD823327 BN25.048G
CX64500 EST710678
CX564990 EST716068
CX564499 EST716077
CX731853 247DBNH U
CO817044 FA_SEAO\(\text{C}\)
CX730532 247DBNH U
CO817044 EST112618
CR973554 EST112618
CB979554 CSA400007
BN687757 BW687757
DN942311 EST113385
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CD834215 BN45.040P
CL516186 SAIL 914
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BH956101 odg94b06.
CB255600 36-E01842
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                                                                                                                                                                                                                                                                                                                                                Description
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Biocceleration Ltd.
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                           GenCore version
Copyright (c) 1993 - 2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  nucleic search, using sw model
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CL516186
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CK264500
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seq length: 200000000
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Contact: Sessions A Applied Trait Genetics Symptomic State Genetics Symptomic Blocchnology Inc.
Symptomic Blocchnology Inc.
Email: allen.sessions@syngenta.com
ABC Stock Number CS841192; T.DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC) sequences represent a pool of amplified genomic regions and not class: TDNA tagged.
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SAIL 914 D07.v2 SAIL Collection Arabidopsis thaliana genomic clone SAIL 914 D07.v2, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            691 GGTAATATCTGGCCTATAATGGGTGCAGGTACCATACAAAACACATATAAAAA 750
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rogids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 963)
357 AIGTIACTCTACACTIGACCAATICAACIGGTICCTCTCTTTIGTTTACATCGTGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                        2442 ATACTICAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCATAACA
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                                                                                                                                                                                                 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAAGAAAAAAACACTCTCCC
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Arabidopsis thaliana (thale cress)
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BN45:040P13F011019 BN45 Brassica napus CDNA clone BN45040P13, mRNA
GD634215
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                                                                                133 TTAAATATTGTAAGTTTGCTTCATTCGAAATTGTAGCTACAGATCTCAAAGCTCCTCCTG 192
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                        Indels
     Pred. No. 3.5e-70;
0; Mismatches 1;
                                                           1319 TITAAATAAATCCATCGTAACCCTCCACTTCAAAATTCTT
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mol type="mRNA"

/cultivar="Jot Neuf"

/db_xref="taxon:3708"

/clone="RNA5040013"

/tissue_type="seed"

/clone_lib="BNA5"
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Brassica napus
         99.78;
       Best Local Similarity 99.7
Matches 356; Conservative
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Best Local Similarity
Matches 471; Conserv
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Entargica oleracea

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Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 700)

S Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,

Whole genome shotgun reads from Brassica oleracea

Longublished (2002)

Context: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wuscl.edu

Plate: odg94 row: b column: 06

Seg primer: -28RPPOT reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH956101 700 bp DNA linear GSS 01-OCT-2002 odg94b06.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
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/clone="SALK 00869.45.50.x"
/clone="lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                         Query Match 10.2%; Score 299.4; DB 9; Length 328; Best Local Similarity 96.4%; Pred. No. 1.9e-57; Matches 317; Conservative 0; Mismatches 11; Indels 1
           /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
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High quality sequence stop: 551.
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
(bases 1 to 328)
Aloneo,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Frednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                       79 ACACCTGCTAATTAATGAGTTTCCTTTTTTTTTTCAGCAAGTTACCTGTGTTACTTGAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 AAGCTCCTCTTTGGCCATAICTCTCTTAACAAACGCATAGTAACAAACGCATAGTAACACATGACCAAGA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 TGACCCAGAGACTTTAAATAAATCCATCGTAACCCTCCACTTCAAAATTCTTTTAAAAA 258
                                                                              /db_xref="taxon:3702"
/clone="SAIL 914 D07.v2"
/clone lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALK 008569.45.50.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_008569.45.50.x, genomic
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                                                                                                                                                                                                                                     Length 963;
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                  organism="Arabidopsis thaliana"
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11.0%; Score 321; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.6e-62;
Matches 321; Conservative 0; Mismatches 0;
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                                     /mol_type="genomic_DNA"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 bp
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BH846526.1 GI:21417397
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SALL 508 H08.vl SAIL Collection Arabidopsis thaliana genomic clone CL488412.
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Vizidiplantas, Streptophyta; Embryophyta; Tracheophyta;
Bobermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 1016)
Sessions, A., Burke, E., Pereting, G., Aux, G., McElver, J., Patton, D.,
Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D.,
Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B.,
Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.7%; Score 284.4; DB 6; Length 97.7%; Pred. No. 5.2e-54; ative 0; Mismatches 6; Indels
Insert Length: 326 Std Error: 0.00
Plate: 8 row: G column: 10
Seg primer: T7R; CTAATACGACTCACTATAGGGA.
                                                              Location/Qualifiers
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Arabidopsis thaliana

Eukaryora, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Bukaryora; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

II (bases I to 326)

Arabidopsis thaliana CDNA library enriched in transcription factors Arabidopsis thaliana CDNA library enriched in transcription factors

Mupublished (2003)

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planter Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaa@mpiz-koeln.mpg.de
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326 bp mRNA linear EST 31-DEC-2004

SED18428-019-008-G10-T7R MPIZ-ADIS-019 Arabidopsis thaliana CDNA

Clone MPIZp766G108Q 5-PRIME, mRNA sequence.

CB255600
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                    /moi_type="genomic DNA"
/db xref="texcn:3712"
/clone_llb="B.oleracea002"
/note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablio Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                            111
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                                                                                                                                                                                                                                                                                  Length 700;
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83.0%; Pred. No. 3.1e-54;
1ve 0; Mismatches 64;
  'organism="Brassica oleracea"
                                                                                                                                                                                                                     Sequencing Center."
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Best Local Similarity
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BZ384971 327 bp DNA linear GSS 26-NOV-2002 SALK 136266.46.25.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_136266.46.25.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTCTATCTTGTTTTAG 2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicotyledons, rosids, eurosida II; Brassicales, Brassicaceae, Arabidopsis. (bases 1 to 327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2273 ATCTCCAIGCTACCCATCATATGTACAACAAAACACAACTCTCTCTCCATTTGCCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 TCTGGTGCTTCTATATCTATTACCTTAAGCTCAACGTTTACTTCCCCAAAGATTCAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 CTACAAAAAAGGCGATGATTATGCAAATACATGTGGCAATGAAGGCTATGCCTTGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAAATGTTACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGAGTTTATGATTTATTGGGTTCACAAAGAGCTTCATGACATTAAATTTCTCTATAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGAGTTTATGATTTATTGGGTTCATAAAGAGCTTCATGACATTAAATTTCTCTATAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2333 TGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGGTGACTTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --------GGGCTCGCGTTCCATCCTTTGGACGGGATACTTCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2453 TATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCATAACACATCTGAGTCT
                                                                                                                                                                                                                                                                                                                                                 TGTGGTTCTTAGTTCTTTCTTGCTTGGTTTCTTCTATTTTTGTGGTTAGAATCCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                    CTACGAGAAAGGCAATGCTTTTGCAAATATATACGTGGCAATGAAGGCTATGCCTTGGTACA
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                                                                                                                                                                                                                                                            Length 749;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                            Score 281.6; DB 6;
Pred. No. 2.6e-53;
0; Mismatches 69;
and http://genoplante-info.infobiogen.fr)
Location/Qualifiers
1. 749
/organism="Brassica napus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGTTTTTGGAAGGGATATGGACAGCAAGCATC 2546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGGITITIGGGAAGGATATGGACAGCGAGCATC 726
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Arabidopsis thaliana
                                                                              /mol_type="mRNA"

cultivar="Jet Neuf"

db_xref="texton:3708"

clone="BN25047803"

fissue type="seed"

clone_lib="BN25"
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                                                                                                                                                                                                                                                              9.6%;
                                                                                                                                                                                                                                                                                Best Local Similarity 73.0
Matches 419; Conservative
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KEYWORDS
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BZ384971/c
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DEFINITION
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                  Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Email: Blon. Research Triangle Park, NC 27709, USA
Email: allen. Sessions@Syngenta.com
ABRC Stock Number CS821429; T.DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
class: TDNA tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1378 ITTAAATATTGTAAGTTTGCTTCATTCGAAATTGTAGCTACAGATCTCAAAGCTCCTCT 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1558 TITACAACCGAATGGTTCTGAGTCACCTTTTGCCGGTGAATCTATGGGAACCTTTACCAC 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD822918 749 bp mRNA linear EST 10-JUL-2003
BN25.047B03F020109 BN25 Brassica napus cDNA clone BN25047B03, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1438 GTTGGCCATATCTCTCTCTCTAACAAGGCATAGTAACACTTGACCACAGTTTGACTTCTCG 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1498 GCGGTTTCATGCCGCGACTATGGCAGATTATAATGATCAGATCGTCAATGAGACCTCTT 1557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 GCGGTTTCATGGCGGCGACTATGGCAGATTATATAATGATCAGATCGTCAATGAAGACCTCTT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica napus
Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 749)
Genoplante.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 TITACAACCGAATGGTICTGAGTCACCTITTGCCGGTGAATCTATGGGAACCTTTACCAC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                    /mol type="Columbia"
/ecotype="Columbia"
/db xref="taxon:3702"
/clone="SAIL 508 H08.v1"
/clone lib="SAIL Collection"
/note="T-DN left border sequences were isolated using modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 TITAAATATTIGTAAGTTIGCTICTITCGAAATIGTAGCTACAGATCTCAAAGCTCCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 283.8; DB 10;
Pred. No. 8.5e-54;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                    organism="Arabidopsis thaliana"
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CD822918.
CD822918.1 GI:32504858
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                                                                                                                                                                                                                                                                                1. .1016
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Matches 296; Conservative
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AUTHORS
TITLE
JOURNAL
COMMENT
  PUBMED
COMMENT
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CD822918
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CD834242
BN45.041B07F011207 BN45 Brassica napus cDNA clone BN45041B07, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 TCTCCAAGAAAGCAGAGAGAAGCCCTTTTGTTTTGTCTTTCTCTTACAACCCTTTTT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761 GCTTCAAGAAAGCAGAGTGAGAATGCCCAACTTGGGTTTTTGTTCTTGTTTTTGTTGTG 820
                                   93, The Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante 80, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 TGGATTGGATGTTTGGCTCTCTTAAGACCCTCTTTTAGAAGATGTTGACAACAAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 GGTACCATACCATACACCACACTACAAGCACAACTATGGTCACTATACATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 TITACAGGGCTTGCATTCACCCAGTAGACGGGATACTTAAGGCTGTACCGCATGTGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 TIGCCGGGCTIGCGTITCACCCAGIAGATGGGAITCTICAGGCTITACCGCAIGTGAIAG
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               261
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 265.4; DB 6
Pred. No. 1.2e-49;
0; Mismatches 56
                                                                                                                                                                                     1. .482
/organism="Brassica napus"
/mol type="mRNA"
/cultivar="jet Neuf"
/db_xref="taxon:3708"
/clone="BN25048614"
/tissue type="seed"
/clone_lib="BN25"
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CD834242.1 GI:32516182
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Best Local Similarity 84.5%;
Matches 310; Conservative
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Brassica napus
  Contact: Genoplante
Genoplante
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AUTHORS
TITLE
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CD834242
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BN25.048G14F020110 BN25 Brassica napus cDNA clone BN25048G14, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicotyledons, rosida, eurosida, eurosida, eurosida, Erassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 CCATGCCACCCATCATATTACAACAAGCAGAATACACTCTCTCCATTTGCCGGTAAGTG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AAAAGACTTTGTCAGCAGCTGCTTGTACTCCAAATCACATTTTGCATTCCTTATCCATAA 240
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:3702"
/clone="SALK 136266.46.25.x"
/clone="SALK 136266.46.25.x"
/clone="Faz abidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                           Arabidopsis Genome
Unpublished (2001)
Unpublished (2001)
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@ealk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g02580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.5%; Score 278.4; DB 9; Length ilarity 99.6%; Pred. No. 1.2e-52; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AGTAACCAGAAAGGCTAGAATTATATAAATGTCAGCTGCA 280
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                                                                                                                                                                                                                                                                                                                                          1. 327
/organism="Arabidopsis thaliana"
/mol_type="genomic_DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                            Class: TDNA tagged.
Location/Qualifiers
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Brassica napus
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Best Local Similarity
Matches 279; Conserv
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CD823327
                                                                                     JOURNAL
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1 (bases 1 to 869)

S Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)

Other_ESTs: EST710577

Contear: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: GTA ATA GGG CC.
                                                                                                                                                                                                                                                                                                                                                                      2081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAAGCAAAACACCTCTCTCC 2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 GCCTIGGTAIACACTTTTCCCAACTGTCTCTGAGTAIATGAICGAGCGTGGTTGGACCAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 ATGTTACTCTACACTTGACCAATTCAACTGGTTCCTCTGTTTTTGTTTACATCGTGCTCTA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 TCTTTTATAGTTGAGTTTGGTATGTATTTGGTTCACAAAGGGCTTCATGACATGACATTAAATT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 TCTCTATAAGCATCTCCATGCCACCCACCACATGTACAACAACAACAACACCTCTCC 535
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        236 AGATTCTATTCCTACAAGAAAGGCAATGATTCAGCAAATACATGTGGCAGTGAAGGGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                2082 GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA
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                                                                                                                                                                                                                                                                                             Length 644;
                                                                                                                                                                                                                                                                                                                               37; Indels
                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                           Score 249.8; DB 6
Pred. No. 4.8e-46;
0; Mismatches 37
                                                                                           1. .644.
/mol type="mRNA"
/mol type="mRNA"
/cultivar="det Neuf"
/db xref="taxon:3708"
/clone="mR45041807"
/tisue type="seed"
/clone_Tib="BN45"
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Solanum tuberosum
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Best Local Similarity 88.0%;
Matches 272; Conservative
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Best Local Similarity
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COMMENT
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KEYWORDS
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ò 용 1. .869 /organism="Solanum tuberosum"

/mol_type="mRNA"

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//IDD LOSE="Displaying stress cDNA library"
//IDD LOSE="Displaying and lost of the library"
//IDD LOSE | IDD CALCO abiotic stress cDNA library"
//IDD CALCOT: DCWNSport6.1; Site | 1: ECORI; Site | 2: Noti; supplier: Solanum tuberosum var. Kennebbe plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mm Nacl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were grown under the standard conditions and 5d). Set 3 were grown under the standard conditions and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, at then were the stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d, 3d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and Arm each heat stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."
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/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2142 ATGITACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTA 2201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACATAGCACTCATATTCCTGGAAGCCTTATGGACAGCTAATATTCATGACAGCTACAT 336
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CK264499
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/clone="POACQ30"
/tiseue_type="abiotic stress treated leaf and root tissue"
/tiseue_type="abiotic stress treated leaf and root tissue"
/lab host="bulloB-Touta"
/clone_lib="potato abiotic stress cDNA library"
/clone_lib="potato a l6hr light/8 hr dark cycle at 25
cfor 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mm Nacl and tissues were harvested at
following application of the sall stress (leaves: 2hr,
6hr, 12hr, ad, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then were cold stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and hoat-stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."
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Solanum tuberosum (potato)
Solanum tuberosum
Solanum tuberosum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Sulantids; lamiids; Solanales; Solanacea; Solanum.
El (bases I to 220)
Suell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from abiotic stressed potato tissue
Lu Unpublished (2003)
Other ESTs: EST716069
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tig.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                           CK269990 920 bp mRNA linear EST 03-AUG-2004 EST716068 potato abiotic stress CDNA library Solanum tuberosum CDNA clone POACQ30 5' end, mRNA sequence.
                                               2681
                                                                                         216
35 GGTAAGGTGTGGCCTGTAATGGGTGCCGGCTATCATACCATTCACCATACAACATACCGC 276
                                        CATAACTATGGTCATTATACCATATGGACTGGATGGTTTGGCTCTCTTATGGTTCT
                                                                         /organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Kennebec"
                                                                                                                                      2682 TTAGCAGAAAAGACA 2697
                                                                                                                                                                                                                                                                                                                                                                                          CK269990.1 GI:39826968
                                                                                                                                                                                 215 GTTGAAGAGGATGCCA 200
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7.8%; Score 228.4; DB 7; Length 920; 62.7%; Pred. No. 4e-41;

Query Match Best Local Similarity

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924 bp mRNA linear EST 03-AUG-2004 EST70577 potato abiotic stress cDNA library Solanum tuberosum cDNA CLONE POABT06 5' end, mRNA sequence.
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1 (Dassa 1 to 934)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTS from abiotic stressed potato tissue Other ESTS: EST10578

Contact: Robin Buell
The Institute for Genomic Research
The Institute for Genomic Research
Fig. Medical Center Dr., Rockville, MD 20850, USA
Email: potato-array@tigr.org
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Solanum tuberosum
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753 bp mRNA linear EST 14-MAY-2005
24RDBNH UP 023 G12 12JAN2004 084 Brassica napus 24RDBNH Brassica
napus cDNA 5′, mRNA sequence.
                                                                                                                                          2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTA 2201
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                                                                                                                                                                                                                                                                               /clone lib="Brassica napus 24RDBNH"
/rote="Vector: pDNR-LIB_CREATOR; Site_1: Sfi I A; Site_2: Sfi I B; Zygotic embryos at heart stage from Brassica napus seeds were used for the isolation of PolyA RNA and in the construction of the cNNA library. Sequences have been trimmed to remove vector and low quality regions using LUCY sequence cleanup software (www.tigr.org)."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                 2622 CATAACTATGGTCATTATACCATATGGATGGACTGGATGTTTGGCTCTCTTATGGTTCCT
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                                    1 (bases 1 to 753)
Xiang, D., Venglat, P., Keller, G., Selvaraj, G. and Datla, R.
Gene Expression Patterns during Brassica Zygotic Embryogenesis
Unpublished (2004)
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Molecular and Developmental Genetics
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 9.9e-41;
0; Mismatches 79;
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/mol_type="mRNA"
/db_xref="taxon:3708"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Raju.Datla@nrc-cnrc.gc.ca
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Location/Qualifiers
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ilarity 69.2%;
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Fax: 306 975 4839
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                                                                                                                                                                                                                                                              /tissue type="abiotic stress treated leaf and root tissue"
/lab_host="ubuloB-rong"
/lab_host="bulloB-rong"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pGWNSport6.1; Site_I: BCORI; Site_2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set I involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Colid
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTAT 2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2082 GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTGTTTTAGTTGAGTTTATGATTTATTGGGTTCACAAAGAGCTTCATGACATTAAATT 2261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTTA 2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2322 ATTTGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGG 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2442 ATACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCTCATAACA 2501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 GCCGTGGTACTGTGCCCTTCCATCACTTTCTGAATACATGATTGAAAACGGATGGACCAA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 rcrigiaaraciecacrirceaarcracrecarecacaagrecarerrecareares 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         578 TCTGTACAAATATCTGCATGCTACACATCATATTTACAACAAGCAAAACACTTTCCCC 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GCATTCCACCCATTGGATGGA 671
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Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/ .
Seg primer: ATT TAG GTG ACA CTA TAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%; Score 227; DB 7; Length 924;
62.7%; Pred. No. 8.3e-41;
iive 0; Mismatches 165; Indels 86; Gaps
                                                                                                                                  /organism="Solanum tuberosum"
/mol_type="mRNA"
/culfivat="Kennebec"
/db xref="taxon:4113"
/clone="POABT06"
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.7
Matches 422; Conservative
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                                                                                    FEATURES
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	CATCTAGGTCTTTTGTTTTATGGAAGCGATATGGACAGCGAACATCCATGACTGCA 753	669	q
	CATCTGAGTCTTTTGTTTTTGGAAGGGATATGGACAGCAAGCA	2502	ò
	ATACTTCAAGCTGTACCGCACGTGGTTGCTTTATAGTGCCGATTCATTTCACAACC 698	639	qq
	ATACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCATCATAACA 2501	2442	ò
	GGGCTTGCGTTTCACCCACTAGACGGG 638	612	q
	TGACTICITIACITGATGITITICGGGTITITCAGGGCTCGCATICCATCCGCTGGACGGG 2441	2382	È
	CTTTGCC	605	qq
	ATTIGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGG 2381	2322	È
	TCTCTATAAGTATCTCCCATGCCACCCATCATATCTACAAACAA	545	qq
	TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAAGCAAAAAAAA	2262	ò
	TCTTGTTTTAGTCGAGTTTTGGTATTTATTGGATGCACAGAGAGCTTCATGACATTAAGCC 544	485	qq
	TCTIGTTTTAGTTTAGAGTTTATTGGGTTCACAAAGAGCTTCATGACATTAAATT 2261	2202	È

Search completed: March 7, 2006, 12:18:47 Job time: 11155 secs

us-10-736-318-22.rni

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March 7, 2006, 09:11:04; Search time 504 Seconds (without alignments) 10316.206 Million cell updates/sec
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5.1.7
Biocceleration Ltd.
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| Cgn2 6/ptodata/1/ina/1_COMB.seq:*
| Cgn2 6/ptodata/1/ina/5_COMB.seq:*
| Cgn2 6/ptodata/1/ina/6_COMB.seq:*
| Cgn2 6/ptodata/1/ina/6_COMB.seq:*
| Cgn2 6/ptodata/1/ina/H COMB.seq:*
| Cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
| Cgn2 6/ptodata/1/ina/RB COMB.seq:*
| Cgn2 6/ptodata/1/ina/RB COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                   1303057 seqs, 888780828 residues
GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             - nucleic search, using sw model
                                                                                                                                                                                                                                                                                    IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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2925
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                                                                                                                                                                                                                                                                                                                                                                                                                                    seq.
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Maximum DB
                                                                                                                                                                                                                                                Sequence:
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                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

643 TTTCCCGGGCTTGCATTTCACCCAGTAGACGGGATACTTCAGGCTGTACCGCATGTGATA 702

462 TTTACAGGGCTTGCA-TTCACCCAGTAGACGGGATACTTAAGGCTGTACGCATGTGATA

Gape

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Length 1175; 10; Indels

Query Match 15.8%; Score 461; DB 3; Best Local Similarity 97.6%; Pred. No. 3e-108; Matches 489; Conservative 0; Mismatches 10

; TYPE: DNA ; ORGANISM: Arabidopsis thaliana US-09-885-723-23

GCGCTG-TTATAGTGCCAATTCATTTCACAACTCATATAGGTCTTTTGTTCATGGAAGCG 703 GCGCTGTTTATAGTGCCAATTCATTCACAACTCATATAGGTCTTTTGTTCATGGAAGCG

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ATATGGACGGCGAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA

580 763 640

639 822 669 882

7458, Ap 14, Appl 15, Appl 1357, Appl 1318, Ap 22, Appl 1280, Ap 901, App 53, Appl 29, Appl 23, Appl 25, Appl 9, Appli 4514, Ap 379, App 13, Sequence 23, Description Sequence Seq Sequence Sequence US-09-443-041A-27 US-09-443-041A-29 US-09-443-041A-23 US-09-443-041A-9 US-09-413-041A-9 US-09-313-294A-4514 US-09-313-294A-74514 US-09-443-041A-13 US-09-443-041A-11 US-09-443-041A-11 US-09-443-041A-15 US-09-443-041A-15 US-09-902-540-1318 US-09-902-540-1318 US-09-902-540-1357 US-09-902-540-138 US-09-885-723-23 SUMMARIES Query Match Length DB 11175 12447 12447 13118 10070 2300 2300 2459 4459 4459 4459 11111 11141 Result υ

AGCTTCAAGAAAGCAGAGGAGGATGCCCACTTGGGGGTTGTTCTTCTGTGTTGTTCTTGT 1002

GTTGTTGTTCAAAGTTTCAGCCTTTCTTGTTCTTTTTCTTCTTCTTCTTATCATGT 879

819

ATGGATTGGATGTTTGGCTCTTTAGGGATCCTCTTAGAAGAAGATGACAACAAAGAC 759 883 ATGGATIGGATGTTTGGCTCTTAGGGATCCTCTTTAGAAGAAGATGACAACAAAGAC 942

900

823

760 943 820

GGATACCATACGATACACCACACACATACAAGCATAACTATGGTCATTATACCATATGG

GGATACCATACGATACACCACACGACATACAAGCATAACTATGGTCATTATACCATATGG

υ	25	53.8	1.8	240	N	US-08-628-417-6	-417-6	Sequence 6, Appli	
U	56	53.2	1.8		٣	US-09-806-708B-22	-708B-22	Sequence 22, Appl	
U	27	52.8	1.8	4167	٣	US-09-973-278-700	-278-700		
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Ü	30	51.4	1.8		~	US-09-014-969-14	-969-14	•	
	31	51.2	1.8	1098	m	US-09-614-221A-113	-221A-113		
U	32	50.8	1.7		٣	US-09-835-811-1	-811-1		
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υ	34	49.4	1.7	41	ო	US-09-949-	US-09-949-016-17091		
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	37	48.6	1.7	2	~	US-07-867-106-2	-106-2		
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U		47.6	1.6		m	US-09-248-	US-09-248-796A-5211	5211,	
						ALIGNMENTS	SINTS		
RES	RESULT 1								
-sn	09-88	US-09-885-723-23							
s .	equenc	ce 23, A	pplica	Sequence 23, Application US/09885723	60/	885723			
۰.	atent	Patent No. 6822142	2142						
 	ENERA	GENERAL INFORMATION:	ATION						
•-	APPLI(APPLICANT: Monsanto	neant	o Company	<u>></u>				
•-	TITLE	OF INVE	NTION	TRANSG	ENI	C PLANTS CO	TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF	LEVELS OF STEROID COMPOUNDS	MPOUNDS
••	FILE	FIDE KEFEKENCE: MIC6/83.1	E. M.	C6/83.1	1		9		
•	CURRE	T APPLI	CATIO	N NUMBER	: C	CURRENT APPLICATION NUMBER: US/09/885,723	23		
•-	CURRENT	CURRENT FILING DATE:	ייא לד	E: 2001-06-20	5	-20			
		7 05 050	1 5	00: 00	r				
	200	MB: Pac	encin	SOFIWARE: FACERLIN VERSION 3.0	·	>			
 	7 7	SEQ ID NO 23							
	PENC	LENGTH: LI/5							

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TCTTGTTTTAGTTTATGATTTATGGGTTCACAAAGAGCTTCATGACATTAAATT 2261
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                                      ATACTICAGGCIATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCTCATAACA 2501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522 aracheciaseccararcecicerearrecreterrecreterececearecaerresease 581
710 CATTIGGCCCTCATATICATIGAGGGCGTTIGGACIGCAAATATICAIGATIGCATICAI 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTCTA
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                                                                    770 GGAAAATTGTGGGCCTGTTATGGGTGGTTACCACACACATTCATCACACATATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AGATGCTGTCCTACAGTAGAAGCTATGAAGAAGGAAATAATTGTTGCATCAAAGGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 GIGITICITICATAICAGCGAAGITGGTIGGCCTAIGIACAITAICIATGTGTCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 ACTATACAAGCACCTACATGCAACCCACCACATTTACAACAAGGAGAAATACCCTATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------CTGGACTAGCATTCCATCCATTGGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTAT
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                                                                                                             96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 188; DB 3; Length 12:
Pred. No. 4.2e-38;
0; Mismatches 175; Indels
                                                                                                                                                                                                                                       Sequence 29, Application US/09443041A
Patent No. 6465717
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1129
; OTHER INFORMATION: any nucleotide
US-09-443-041A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 ATTTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 59.81
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
                                                                                                                                                                                                              RESULT 3
US-09-443-041A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1447;
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                                                                                                                                                                                                                                                           Sequence 27, Application US/09443041A
Sequence 27, Application US/09443041A
SEQUENCE 27, Sequence 27, Application US/09443041A
SEQUENCE 27, Sequence 27, APPLICANT: Pamodu, Omolayo O. APPLICANT: Pamodu, Omolayo O. APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE: 1998-10-18
CURRENT FILING DATE: 1998-11-20
FRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOPTWARE: Microsoft Office 97
SEQ ID NO 27
LENGTH: 1447
                                                                                                                                                             940 TANATGITTGATGATCTTTGC 960
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US-09-443-041A-27
                                                            880
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                             468 ACATCGCTCTCGTGTTTTGGAGGGCGTGTGGACGACGACAACATCCACGACTGCATTCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTAT
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58.6%; Pred. No. 6.3e-36;
iive 0; Mismatches 189;
                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/09443041A
Fatent No. 6465717
GENERAL INFORMATION:
GAPLICANT: Famodu, Guddy
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
FRIOR APPLICATION NUMBER: 60/109,283
FRIOR PLILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 5:
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Best Local Similarity 58.6
Matches 389; Conservative
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; ORGANISM: Oryza sativa
US-09-443-041A-25
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                                                                                                      CCTTGGTACACTCTTCCTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAAA 2142
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                                                                                                                                            642 GGCAAGATCTGGCCGGTGATGGGCGCCGGCTACCACCATCCACCACACGACGTACCGG 701
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Best Local Similarity 59.8%; Pred. No. 6.7e-38;
Matches 388; Conservative 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/09443041A
Petent No. 6465717
GENERAL INFORMATION:
APPLICANT: Famedu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR PPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 23
LENGTH: 911
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RESULT 7
US-09-313-294A-4514
i Sequence 4514, Application US/09313294A
j Patent No. 647612
j GENERAL INFORMATION:
j APPLICANT: Lalgudi, Raghunath V.
j APPLICANT: Lalgudi, Raghunath V.
j TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
j FILE REFERENCE: PL-0017 US
j CURRENT APPLICATION NUMBER: US/09/313,294A
j CURRENT FILING DATE: 1999-05-14
j NUMBER OF SEQ ID NOS: 7600
j SOFTWARE: PERL PROGRAM
j SEQ ID NO 4514
j LENGTH: 300
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575 TCTCATTTTTGTGGAGTTTGGAATTTACTGGATGCACAGAGAGTTGCATGACATAAAGCC 634
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; OTHER INFORMATION: Incyte ID No. 6476212 700348549H1
US-09-313-294A-4514
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ORGANISM: Zea mays
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         865 cacaactatrosccactacaccererosatrosacrosaterrosocacecerrosasaseca 924
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Patent No. 6455717
GENERAL INPORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jenni
APPLICANT: Shen, Jenni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jenes
FILE REFERENCE:
CURRENT FILING DATE: 1999-11-18
FRIOR FILING DATE: 1998-11-20
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NAME/KEY: unsure
LOCATION: (885)
OTHER INFORMATION: any nucleotide
NAME/KEY: unsure
LOCATION: (949)
OTHER INFORMATION: any nucleotide
NAME/KEY: unsure
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OTHER INFORMATION: any nucleotide
NAME/KEY: unsure
LOCATION: (1050)..(1051)
OTHER INFORMATION: any nucleotide
NAME/KEY: unsure
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SOFTWARE: Microsoft Office 97
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SEQ ID NO 9
LENGTH: 1070
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Sequence 7458, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPERENCE: PL-0017 US/09/313,294A
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PEL PROGram
SEQ ID NO 7458
LENGTH: 314
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                                                                                                                      Length 459;
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                                                                                                                  Score 90; DB 3; Length 459
Pred. No. 4.1e-13;
0; Mismatches 70; Indels
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; OTHER INFORMATION: Incyte ID No. 6476212 700381763H1
US-09-313-294A-7458
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US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
                                                                                                                      Query Match
3.1%;
Best Local Similarity 66.8%;
Matches 143; Conservative
; ORGANISM: Glycine max US-09-443-041A-13
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ORGANISM: Zea mays
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 379
LENGTH: 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
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CTHER INFORMATION: Incyte ID No. 6476212 700549111H1
NAME/KEY: unsure
LOCATION: S
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-379
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Sequence 13, Application US/09443041A

Patent No. 6465717

GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Refalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1999-11-18
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
LENGTH; 459
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                                          2648 GATGGACTGGATGTTTGGCTCTCT 2671
                                                                                                                  248 garggacrggargrrrggracgcr 271
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Patent No. 6476212
GENERAL INFORMATION:
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ORGANISM: Zea mays
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1602 TGGGAACCTTTACCACATTTCCTCCAGACATGGCTCCGGAACTACCTCGCCGGAAACATA 1661
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70.4%; Pred. No. 3.2e-08;
iive 0; Mismatches 40
                                                                                                                                                                                          APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
APPLICANT: Shen, Jennie
FILE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
                                                                                                             Sequence 15, Application US/09443041A Patent No. 6465717 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: any nucleotide NAME/KEY: unsure LOCATION: (288)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (261)
OTHER INFORMATION: any nucleotide
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OTHER INFORMATION: any nucleotide
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INFORMATION: any nucleotide
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INFORMATION: any nucleotide
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                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
                                                                                                                                                                              APPLICANT: Famodu, Omolayo O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.4
Matches 95; Conservative
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TION: (372)
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LOCATION: (450).
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                                                                                                                                                                                                                                                                       COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSDY disk
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ilarity 6.1%; Pred. No. 1.9e-09;
Conservative 236; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIP CATTON: 435
RIGHARD APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 39,768
RECISTRATION NUMBER: 29,768
RECISTRATION INFORMATION:
TELEFRHONE: (703) 836-9300
TELEFRAX: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base palrs
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STRANDEDNESS: single
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Best Local Similarity
Matches 25; Conserv
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Sequence 1357, Application US/09902540

Sequence 1357, Application US/09902540

Sequence 1357, Application US/09902540

Patent No. 6833447

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Waxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10 (15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

EENGTH: 612
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Best Local Similarity 61.1%; Pred. No. 7.2e-08;
Matches 146; Conservative 0; Mismatches 91; Indels
                                                                                                                               APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TILE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: ungure

| LOCATION: (1)..(612)

| THER INFORMATION: ungure at all n locations

US-09-902-540-1357
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
SEQ ID NO 11
TYPE: DNA
RESULT 13
US-09-443-041A-11
Sequence 11, Application US/09443041A
Patent No. 6465717
GENERAL INFORMATION:
APPLICANT: Pamodu, Omolayo O.
APPLICANT: Orozco, Buddy
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US-09-443-041A-11
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DB 3; Length 612;

2.3%; Score 68;

Query Match

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Patent No. 68334710:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hise, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38.10(15849)B
FILE REPERENCE: 38.10(15849)B
CURRENT APPLICATION NUMBER: 60/99/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
                                                                                       1856 TIGICTICTACTICTCATITAAITAGTITTAAGTITAATATITTTGGCTAATCCACATI
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                   0; Mismatches 137; Indels
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Pred. No. 1.7e-05;
0; Mismatches 149;
 52.1%; Pred. No. 2.1e-07;

   LOCATION: (1)..(614)
   OTHER INFORMATION: ungure at all n locations
US-09-902-540-1318

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Best Local Similarity 52.1
Matches 149; Conservative
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Matches 150; Conservative
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US-09-902-540-1318/c
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Search completed: March 7, 2006, 13:20:15 Job time : 509 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-259-194A-530
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c 29 72 2.5 1179 9 US-10-363-483A-36196 Sequence 36196, A 30 71 2.4 495 6 US-10-24-4880C-1.5 Sequence 15, Appl 31 C 69.4 2.4 6668 6 US-10-24-880C-1.5 Sequence 1670, Appl 32 69.4 2.4 560 6 US-10-24-880C-1.1 Sequence 11, Appl 34 68.6 2.3 2.7 3 US-09-923-876-5279 Sequence 5279, Ap 35 68.6 2.3 2.7 3 US-09-923-876-5279 Sequence 5279, Ap 36 68.4 2.3 431 3 US-09-923-876-5279 Sequence 5279, Ap 36 68.4 2.3 431 3 US-09-923-876-5279 Sequence 5279, Ap 37 68.4 2.3 432 8 US-09-923-876-5279 Sequence 5279, Ap 37 68.4 2.3 432 8 US-09-96-352-5558 Sequence 5279, Ap 37 68.4 2.3 6960 6 US-10-311.455-2372 Sequence 2372, Appl 39 67.2 2.3 428 3 US-09-96-352-573 Sequence 2772, Appl 39 67.2 2.3 428 3 US-09-96-352-573 Sequence 2772, Appl 39 67.2 2.3 428 3 US-09-96-352-573 Sequence 5772, Appl 30 05-252-57
29 72 2.5 1179 9 US-10-363-483A-36196 Sequence 36196 30

ALIGNMENTS	SULT 1 -09-775-879-22 Sequence 22, Application US/09775879 Patent No. US20020668822A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Choe, Sunghwa APPLICANT: Peldmann, Kenneth A TITLE NEPRENCE: 2225-0003 CURRENT APPLICATION NUMBER: US/09/775,879 CURRENT PELLING DATE: 2001-02-02 RIOR APPLICATION NUMBER: 60/179,901 PRIOR FILING DATE: 2000-02-02 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin Ver. 2.0 LENGTH: 2925 LENGTH: 2925 TYPE: DNA OKGANISM: Genomic HDF7 -09-775-879-22	Query Match 100.0%; Score 2925; DB 3; Length 2925; Best Local Similarity 100.0%; Pred. No. 0; Matches 2925; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 GTTTGGTATTTATTGGATGCACAGAGCTTCATGACATTAAGCCTCTCTATAAGTATCT 60	CCATGCCCATCCATATCTACAAGCAGAATACACTCTCTCCATTTGCCGGTAAGTG	61 CCATGCCACCCATCATATCTACAAGAAGAAATACAATTCTCTCTC	121 TITTCAGITTGITCTTCTTAGTTCTTGTAAAGAITGGTAGCATTTAGTTTTACCAG 180	121 Trircagrirgircricriragricrigiaaaagarrogragcarriagrircriaccag 180	181 AAAGACITIGICAGCAGCIGCITGIACICCAAAICACAITITGCAITCCITAICCAIAA 240	181 AAAAGACTTTGTGAGCAGCTGCTTGTACTCCAAATCACATTTTGCATTCCTTATCCATAA 240	241 AGTAACCAGAAAGGCTAGAATTATATAAATGTCAGCTGCATTACTTCACATATGTCAGAG 300	241 AGTAACCAGAAAGGCTAGAATTATATAAAATGTCAGCTGCATTACTTCACATATGTCAGAG 300	
	RESULT 1 US-09-775-879-22 Sequence 22, A Patent No. US2 GENERAL INFORM APPLICANT: CF TITLE OF INVE FILE REFERENC CURRENT APPLICA CURRENT APPLICA CURRENT APPLICA CURRENT FILIN CURRENT FILIN FILE REFERENC SOFTWARE: PAL SEQ ID NO 22 LENGTH: 2925 LENGTH: 2	Query Match Best Local Matches 292	٥٧ اور		Db 60	Ωγ 12	Db 12	Qy 18	Db 18	Qy 24	Db 24	

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100.0%; Score 2925;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2925; Conservative 0; Mismatches
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Publication No. US200401339481
GENERAL INFORMATION:
APPLICANT: Choe, Sunghwa
APPLICANT: Feldmann, Kenneth A
TITLE OF INVENTION: Dwf7 MUTANTS
FILE REFERENCE: 2225-0003
CURRENT FILING DATE: 2003-12-15
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US/09/775,879
PRIOR FILING DATE: 2001-02-02
PRIOR PRILING DATE: 2000-02-02
PRIOR PRILING DATE: 2000-02-02
SOFTWARE: PREATION DATE: 2000-02-02
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, ORGANISM: Genomic HDF7
US-10-736-318-22
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Pred. No. 5.6e-204;
                                                                                                                                                     0; Mismatches
                                      TYPE: DNA ORGANISM: Genomic dwf7 (Arabidopsis)
                                                                                                              Query Match
31.6%;
Best Local Similarity 99.6%;
Matches 958; Conservative
     SEQ ID NO 20
LENGTH: 1889
                                                               ; ORGANISM: GEI
US-10-736-318-20
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CURRENT FILE REPERBNCE: 2225-0003
CURRENT FILING DATE: 2003-12-15
CURRENT FILING DATE: 2003-12-05
PRIOR APPLICATION NUMBER: US/09/775,879
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2000-02-02
PRIOR PILING DATE: 2000-02-02
PRIOR PILING DATE: 2000-02-02
PRIOR FILING DATE: 2000-02-02
SOFTWARE: PATCHT IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN UNITED IN 
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Sequence 421, Application US/09938842A

Fatent No. US20020160378A1

FAPELCANT: HARPET. Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

TITLE OF INVENTION: SARE, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SARE, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR PAPLICATION NUMBER: US 60/227,866

PRIOR PILING DATE: 2000-08-24

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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Best Local Similarity 97.6%; Pred. No. 2.3e-96;
Matches 489; Conservative 0; Mismatches 10; Indels
CURRENT APPLICATION NUMBER: US/10/862,907
CURRENT FILING DATE: 2004-06-07
PRIOR APPLICATION NUMBER: US/09/885,723
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERBION 3.0
SEQ ID NO 23
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; ORGANISM: Arabidopsis thaliana
US-10-862-907-23
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US-09-938-842A-421
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Sequence 23, Application US/09885723

Sequence 23, Application US/09885723

Sequence 23, Application US/09885723

Sequence 23, Application US/09881

Sequence 23, Application US/09081

GENERAL INFORMATION:

TATLE OF INVENTION:

TRANGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS

TITLE OF INVENTION:

TOTRENT PELLICATION NUMBER: US/09/885,723

CURRENT FILING DATE: 2001-06-20

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 23

LENGTH: 1175
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Publication No. US20050086713A1
GENERAL INFORMATION:
APPLICANT: MONBENIC COMPANY
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS
FILE REFERENCE: MTC6783.1
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Pred. No. 5.7e-70;
0; Mismatches 108;
CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR PELING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR PRIOR FILING DATE: 2001-06-22

SEQ ID NO 421
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                                                                                                                                                                    TYPE: DNA ORGANISM: Arabidopsis thaliana
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Best Local Similarity 72.4%;
Matches 508; Conservative
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Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Right Application STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
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US-09-938-842A-421
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NUMBER OF SEQ ID NOS:
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TYPE: DNA
ORGANISM: Sorghum bicolor
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APPLICANT: Orozco, Emil M.
APPLICANT: Refalski, J. Antoni
APPLICANT: Refalski, J. Antoni
APPLICANT: Refalski, J. Antoni
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE: BB1282 US DIV
CURRENT PELLIG DATE: 2002-08-21
PRIOR PILLIG DATE: 2002-08-21
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 27
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Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Glycine max
US-10-224-880C-27
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILE REPERBINES: 38-21 (53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT PILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 13122 LENGTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS11413_1
US-10-767-701-13122
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Publication No. US20040010815A1
GENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Lange, Markus B.
APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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2082 GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Moughamer, Todd
APPLICANT: Provatt, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
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CURRENT FILING DATE: 2003-01-07
FRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PATENTISELISE. DIOS: 662
                                                                                                                                                                                                        Sequence 530, Application US/10259194A Publication No. US20040010815A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               APPLICANT: Lange, Markus B.
APPLICANT: Chassemian, Majid
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Gooff, Stephen A.
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Pumiyaki
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Best Local Similarity 59.8%;
Matches 389; Conservative
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; ORGANISM: Triticum aestivum
US-10-259-194A-530
         TAG 2685
         2683
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                                                                                                                                                                                                               PLANT GENES
                                                                             APPLICANT: ALGED, COCA APPLICANT: ALGED, COCA APPLICANT: ALGED, COCA APPLICANT: Provart, Nicholas APPLICANT: Provart, Nicholas APPLICANT: Zhu, Tonart, Nicholas APPLICANT: Zhu, Tonart, Dentril Zhu, Tonart Zhu, Tonarell Zheke, Darrell Zheke, Darrell Zheke, Darrell Zheke, Tonarell Zheke, Tonarell Zheke, Dentril Zheke, Tonarell Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Dentril Zheke, Den
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Pred. No. 2.7e-33;
0; Mismatches 191;
Stephen A.
iri, Fumiyaki
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Best Local Similarity 59.3%;
Matches 393; Conservative
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Pred. No. 1e-32;
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US-10-224-880C-23
Sequence 23, Application US/10224880C
Sequence 23, Application US/10224880C
Publication No. US20030229914A1
GENERAL INFORMATION:
APPLICANT: Famedu, Omolayo O.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Shen, Jennie B.
TITLE NOFINVENTION: Sterol Metabolism Enzymes
FILE REFERENCE: BB1282 US DIV
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR PILING DATE: 1999-11-20
NUMBER: OF SEGID NOS: 33
SOFTWARE: Microsoft Office 97
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Best Local Similarity 59.8
Matches 388; Conservative
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; ORGANISM: Zea mays
US-10-224-880C-23
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59.8%; Pred. No. 7e-33;
tive 0; Mismatches 175; Indels 8
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| Publication No. US20030229914A1
| GENERAL INFORMATION:
| APPLICANT: Famodu, Omolayo O. APPLICANT: Rafalski, J. Antoni
| APPLICANT: Rafalski, J. Antoni
| APPLICANT: Rafalski, J. Antoni
| APPLICANT: Rafalski, J. Antoni
| APPLICANT: Rafalski, J. Antoni
| APPLICANT: Rafalski, J. Antoni
| APPLICANT: Rafalski, J. Antoni
| APPLICANT: Shen, Jennie B. TITLE REFERENCE: BB1282 US DIV
| TITLE REFERENCE: BB1282 US DIV
| CURRENT APPLICATION NUMBER: 60/109,283
| PRIOR APPLICATION NUMBER: 60/109,283
| SOFTWARE: Microsoft Office 97
| SEQ ID NO 29
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-----TGGACTCGCGTTTCACCCACTGGATGGTA 407
                                                                           408 TTCTGCAAGCGATACCGCATGTGCTTTGCTTCCTCCTCCCAACGCACTTCAGAACGC
                                                                                                                                      2443 TACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCATAACAC
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APPLICANT: Kreps, Joel
APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REPERENCE: 70029-NP
CURRENT APPLICATION UNMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.3%; Score 184.4; DB 6; Length 828; Best Local Similarity 59.0%; Pred. No. 4e-32; Matches 392; Conservative 0; Mismatches 186; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                           2623 ATAACTAIGGICATTATACCATAIGGAIGGACTGGAIGTTIGGCICICT 2671
                                                                                                                                                                                                                                                                                                                                                         588 ACAACTAIGGCCACTACACCGICIGGAIGGACTGGAIGTIIGGIACGCI 636
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PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR FILING DATE: 2001-09-26

PRIOR PAPLICATION NUMBER: US 60/370,743

PRIOR PELICATION NUMBER: US 60/370,620

PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04

NUMBER OF SEQ ID NOS: 662

SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta

SEQ ID NO 608

LENGTH: 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 608, Application US/10259194A
Publication No. US20040010815A1
GENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Grassemian, Majid
APPLICANT: Cooper, Bret
APPLICANT: Gooper, Bret
APPLICANT: Gooper, Grassemian, Applicant:
APPLICANT: Gooff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
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2: /cgn2_6/ptodata/1/pubpna/USOG_NEW_PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Seguence 337713,	Sequence 749620,	Sequence 822274,	Sequence 12, Appl	34,	Sequence 599143,	Sequence 80, Appl	Sequence 182, App	Sequence 10, Appl	Sequence 133, App	Sequence 278, App	Sequence 33, Appl	Sequence 714408,	Sequence 714409,	Sequence 714410,	Seguence 714411,	Sequence 96, Appl	Sequence 939011,	Sequence 79, Appl	Sequence 2, Appli	Seguence 40, Appl	Sequence 162822,	Sequence 71, Appl	Sequence 808614,	Sequence 41, Appl
US-09-925-065A-337713	US-09-925-065A-749620	US-09-925-065A-822274	US-10-240-708-12	US-10-240-708-34	US-09-925-065A-599143	US-10-240-708-80	US-11-091-883-182	Þ	US-10-947-249-133	US-11-000-688-278	US-10-240-708-33	US-09-925-065A-714408	US-09-925-065A-714409	US-09-925-065A-714410	US-09-925-065A-714411	US-11-011-332A-96	US-09-925-065A-939011	US-10-240-708-79	US-10-240-708-2	US-10-240-708-40	US-09-925-065A-162822	US-10-240-708-71	US-09-925-065A-808614	US-10-240-708-41
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1.7	1.7	1.7	1.7	1.7	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6
48.8	48.8	48.8	48.6	48.4	48	47.8	47.6	47.4	47.2	47.2	47.2	47	47	47	47	47	46.8	46.8	46.8	46.8	46.6	46.6	46.4	46.4
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ALIGNMENTS

RESULT 1 US-112-026A-181 US-11-102-026A-181 Sequence 181, Application US/11102026A Publication No. US20060021087A1 GENERAL INFORMATION: APPLICANT: Monsanto Technology LLC APPLICANT: Gilbertson, Larry A APPLICANT: Gilbertson, Larry A APPLICANT: Lux Maolon APPLICANT: Lux Maolon APPLICANT: Lux Maolon APPLICANT: Lux Maolon APPLICANT: Moberts, James K APPLICANT: Roberts, James K APPLICANT: Roberts, James K APPLICANT: Roberts, James K APPLICANT: Roberts, James K APPLICANT: Roberts	
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Query Match 1.9%; Score 54.2; DB 12; Length 3641; Best Local Similarity 50.6%; Pred. No. 0.81; Matches 131; Conservative 0; Mismatches 128; Indels 0; Gaps 0;	

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Sequence 4.2 Application US/10240708
| Publication No. US20050282157A1
| GENERAL INFORMATION:
| APPLICANT: DIER, Alexander
| APPLICANT: DIERENBROCK, Christian
| APPLICANT: PIEPENBROCK, Christian
| APPLICANT: BERLIN, Wart
| TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
| TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
| TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
| TITLE OF INVENTION: By Assessing DNA Methylation
| FILE REFERENCE: 5013.1012
| CURRENT FILING DATE: 2002-10-03
| PRIOR APPLICATION NUMBER: DE 10019058.8
| PRIOR PELING DATE: 2000-04-06
| PRIOR FILING DATE: 2000-04-06
| PRIOR FILING DATE: 2000-04-06
| PRIOR FILING DATE: 2000-04-06
| PRIOR FILING DATE: 2000-04-06
| PRIOR FILING DATE: 2000-06-30
| PRIOR FILING DATE: 2000-06-30
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Publication No. US20050282157A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFRENCE: 5013.1012
CURRENT FILING DATE: 2002-10-03
FRICA APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2001-04-06
FRICA APPLICATION NUMBER: DCT FR01/03971
FRICA RAPLICATION NUMBER: DCT FR01/03971
FRICA APPLICATION NUMBER: DCT FR01/03971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 ATTTAAAAAGTTGATTTTGGCGGGGGGGGGGTTTAATGTTTGGGATTTTAGTAT 309
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1971 TTTGTGGTTCTTAGTTCTATTTCTTGCTTGGTTTCTTCTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.6%;
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-240-708-42
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OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
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                                                                                            TITCAGITCTTGICTTCTACTICTCATTTAATTAGTTTTAAAGTTTAATATTTTTGGCTA 1906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13236, Application US/10995561
Sequence 13236, Application US/10995561
Sequence 13236, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: 103/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FactSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1674 TCCGGCTTCCTCTGGTGCTTCTACATCTATTACCTTAAACTCAACGTTTACGTCCCCAAA 1733
140976 igcrccciccarngrggcrrrgcaacarrrarrrrarrrarrrrrrrarrarrrra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTGTCTTCTACTTCTCATTTAATTAGTTTTAAAGTTTTAATATTTTTGGCTAATCCACA
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49.3%; Pred. No. 3.4;
tive 0; Mismatches 172; Indels 1;
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Matches 168; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (1)...(30531;
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LENGTH: 305312
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Matches 138;
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         Query Match
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APPLICANT: DLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: DASSESSING DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: DS/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
LENGTH: 6326
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                                                                                                                                                                                                                                                   ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-708-63
                                                                                                                                                                                                                                                                                                            DB 8; Length 5562
                                                                                                                                                                                                                                                                                                          Query Match 1.8%; Score 52; DB 8; Length 556
Best Local Similarity 50.7%; Pred. No. 2.4;
Matches 150; Conservative 0; Mismatches 145; Indels
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
SEQ ID NO 63
LENGTH: 5562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 57, Application US/10240708 Publication No. US20050282157A1 GENERAL INFORMATION:
                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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US-10-240-708-57
                                                                                                                                                                                               TYPE: DNA
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RESULT 6
US-10-240-708-72

US-10-240-708-72

Sequence 72, Application US/10240708

PUBlication No. US20050282157A1

GENERAL INFORMATION:

APPLICANT: DIEEK, Alexander

APPLICANT: DIEEK, Alexander

APPLICANT: DIEEKLINK ENT.

ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

ITILE OF INVENTION: DATE: 2002-10-03

PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR PLICATION NUMBER: DE 10019173.8

PRIOR PLICATION NUMBER: DE 10032529.7

PRIOR PLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SEXUENCE OF SEQ ID NOS: 98
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                                                                                                          1740 TITITICAATITCGAIGITCTGTTTTGAAACCTTTCTTTTGTTGATTCCTTCGATTGTAT
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-72
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  Length 6326;
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                                                        Indels
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Pred. No. 3.2;
0; Mismatches 139;
Score 51.6; DB 8;
Pred. No. 3;
                                                     0; Mismatches 144;
  1.8%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 51.0%;
Matches 146; Conservative (
                                                     Conservative
                            Similarity
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ATCTTCCATGAAATTTGAGCTCAAAATATACCATGAA-ATTGAAATTTGTGGTTCTTAGT 1985
                                                 1654 GAAACATACTCTACTTCATCTCCGGCTTCCTCGGTGCTTCTACATCTATACCTTAAAC 1713
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                                                                                                                                                                                                                                                                                                                            FULLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Unclected Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2001-11-30

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

SOFTWARE FEASTER OF WINDER: US 60/289,846

PRIOR FILING DATE: 2001-01-6

SEQ ID NOS: 957086

SEQ ID NO 768903

LENGTH: 628
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US-09-925-065A-402424/c

Sequence 402424, Application US/09925065A

Spinitration No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TILLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A
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                                                                                                     TCTATTTCTTGCTTGGTTTCTTCTATTTTTGTGGTTAGAATCCATT 2031
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Best Local Similarity 51.7%; Pred. No. Matches 140; Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                   Sequence 768903, Application US/09925065A Publication No. US20040181048A1
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US-09-925-065A-768903
1927
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196 GTAICGCCTGATAGATIGIGITATACGITAACCTTTTTTTTTCTTACTGTTACTTTCAGTTC 1855
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sequence 402425, Application US/09925065A
sequence 402425, Application US/09925065A
sublication No. US2004018104811
general information:
general information:
string of information:
string of invention:
string of invention:
string application information:
string application with the Human Genome
string application Number: US/09/925,065A
current application Number: US/09/925,065A
current filing date: 2000-10-4
string application Number: US 60/243,096
string application Number: US 60/252,147
string application Number: US 60/250,092
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CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SEQ ID NO 402424

LENGTH: 664
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 402425
LENGTH: 664
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Best Local Similarity 48.0
Matches 142; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-402424
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US-09-925-065A-402425
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   TGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTGAAATTTGTGGTTCTTA 1983
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                                                                          Sequence 834303, Application US/09925065A

Fublication No. US20040181048A1

FUBLICANT: Wang, David G.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE REPERENCE: 108627.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

FRIOR PRING DATE: 2000-10-24

FRIOR PILING DATE: 2000-11-24

FRIOR APPLICATION NUMBER: US 60/252,147

FRIOR APPLICATION NUMBER: US 60/250,092

FRIOR APPLICATION NUMBER: US 60/250,092

FRIOR PILING DATE: 2001-11-16

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-05-09

FRIOR FILING DATE: 2001-05-09

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51.7%; Pred. No. 3.3;
tive 0; Mismatches 127;
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                                                                                                                                                                                                                                                                                      2044 GCAATGCTTTTGCAAATAT 2062
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Matches 140; Conservative
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US-09-925-065A-834303
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sguence 66, Application US/10240708

publication No. US20050282157Al

general INFORMATION:

publication No. US20050282157Al

general INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: OLEN, Rutt

TITLE OF INVENTION: Dy Assessing DNA Methylation

TITLE OF INVENTION: Dy Assessing DNA Methylation

FILE OF INVENTION: Dy Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/240,708

CURRENT FILING DATE: 2002-10-03

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR PILING DATE: 2000-04-06

PRIOR PLING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR PILING DATE: 2000-04-07

PRIOR PLING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

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ilarity 47.3%; Pred. No. 5.2;
Conservative 0; Mismatches 168; Indels 0
Score 50.8; DB 6; Length 664;
Pred. No. 2.2;
1; Mismatches 153; Indels
Match 1.7%;
Local Similarity 48.0%;
les 142; Conservative 1
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Best Local Similarity
Matches 151; Conserv
   Query Match
Best Local S:
Matches 142
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RESULT 14

US-10-240-708-47

US-10-240-708-47

Sequence 47, Application US/10240708

Publication No. US20050282157A1

SEQUENCE 47, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: PIEBRNBROCK, Christian

APPLICANT: PIEBRNBROCK, Christian

APPLICANT: PIEBRNBROCK, Christian

APPLICANT: PIEBRNBROCK, Christian

APPLICANT: DERLIN, Kurt

TITLE OF INVENTION: Dy Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT PELING DATE: 2002-10-03

PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR PLICATION NUMBER: DE 10019058.8

PRIOR PLICATION NUMBER: DE 10019058.8

PRIOR PLICATION NUMBER: DE 10019058.8

PRIOR PLICATION NUMBER: DE 10019058.8

PRIOR PLING DATE: 2000-04-07

PRIOR PLING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SEQ DI NO 477

LENACH. ELENA
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                                                                                                                                                                                                                                                                                                      1353 AACCTCACCATATTTGGAAGATTCCTACTCCATTTGCAAGTCATGCTTTTCACCCTATTG 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1293 ArGGCTTTCTTCAGAGTCTACCTTACCATATATACCCTTTTATTTCCATTACACAAGG 1234
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                                                                            2317 TCTCCATTTGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATC
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                                                                                                                                                                                                                                                                                                                                                                                       2437 ACGGGATACTICAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCCGATTCATCTCA
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                                                                                                                                                                                                                                  2377 AATGGTGACTICTTTACTTGATGTTTTTCGGGTTTTCAGGGCTCGCATCCGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8; Length 5152;
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1.7*; Score 49.4; DB 8; Length 5;
Best Local Similarity 50.4*; Pred. No. 7.3;
Matches 119; Conservative 0; Mismatches 117; Indels
Mismatches 116; Indels
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ORGANISM: Artificial Sequence
    Conservative
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LOCATION: (67, 20
    Matches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1654 GAAACATACTCTACTTCATCTCCGGCTTCCTCTGGTGCTTCTACATCTATTACCTTAAAC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1714 TCAACGTTTACGTCCCCAAAGGTTACTTTTTTCAATTTCGATGTTCTGTTTTGAAACCTT 1773
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Sequence 2, Application US/10821234;
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan,
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
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APPLICANT: Nawher 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 a
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    TITLE OF INVENTION: Identification and Mapping of Single ITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.4; DB 8; Length 2409;
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7%; Score 49.4; DB 6; Length 613; ilarity 51.3%; Pred. No. 4; Conservative 1; Mismatches 127; Indels
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                                                    TITLE OF INVENTION: NUCLECLING FOLYMORE INCREMENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 PRIOR PILING DATE: 2001-08-08 PRIOR PLING DATE: 2000-10-24 PRIOR PLING DATE: 2000-10-24 PRIOR PLING DATE: 2000-11-20 PRIOR PLING DATE: 2000-11-30 PRIOR PLING DATE: 2000-11-30 PRIOR PLING DATE: 2000-11-30 PRIOR PLING DATE: 2001-01-16 PRIOR PLING DATE: 2001-01-16 PRIOR PLING DATE: 2001-01-16 PRIOR PLING DATE: 2001-05-09 NUMBER: US 60/289,846 PRIOR PLING DATE: 2001-01-16 PRIOR PLING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 957086 SEQ ID NO 934302 LENGTH: 61
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ORGANISM: Homo sapiens
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US-09-925-065A-834302
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Best Local Similarity
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Matches 139; Conserv
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1.7%; Score 49.4; DB 12; Length 10166;
Best Local Similarity 49.4%; Pred. No. 8.9;
Matches 128; Conservative 0; Mismatches 131; Indels 0;
                          Sequence 3, Application US/11147606
| Publication No US20050278795A1
| GENERAL INPORMATION:
| APPLICANT: Ntambi, James M.
| APPLICANT: Ntambi, James M.
| APPLICANT: Miyazaki, Makoto
| TITLE OF INVENTION: Stearoyl-COA desaturase 4 gene
| FILE REFERENCE: 960296.00197
| CURRENT PILING DATE: 2005-06-08
| PRIOR PILING DATE: 2004-06-09
| PRIOR PILING DATE: 2004-06-09
| SOFTWARE: PatentIn Version 3.2
| SEQ ID NO 3: 13
| LENGTH: 10166
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                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Mus musculus
US-11-147-606-3
RESULT 15
US-11-147-606-3
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Search completed: March 7, 2006, 09:42:29 Job time : 811 secs

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